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Input file Fbh2786c.seq; Output File 2786.trans  
Sequence length 2459

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E H S P G S G A A R R P L H S A <sup>162</sup> O A V D										24
GAG CAT TCC CCC GGC AGC GGC GCG GCC CGG CGG CCG CTG CAC TCC GCG CAG GCT GTG GAC										72 133
V A S A S N F R A F E L L H L H L D L R										44
GTG GCC TCG GCC TCC AAC TTC CGG GCC TTT GAG CTG CTG CAC TTG CAC CTG GAC CTG CGG										132 193
A E F G P P G P G A G S R G L S G T A V										64
GCT GAG TTC GCG CCT CCA GGG CCC GGC GCA GGG AGC CGG GGG CTG AGC GGC ACC GCG GTC										192 253
L D L R C L E P E G A A A E L R L D S H P										84
CTG GAC CTG CGC TGC CTG GAG CCC GAG GGC GCC GCC A G CTG CGG CTG GAC TCG CAC CCG										252 313
C L E V T A A A L R R E R P G S E E P P										104
TGC CTG GAG GTG ACG GCG GCG GCG CTG CGG CGG GAG CGG CCC GGC TCG GAG GAG CCG CCT										312 373
A E P V S F Y T O P F S H Y G O A L C V										124
GCG GAG CCC GTG AGC TTC TAC ACG CAG CCC TTC TCG CAC TAT GGC CAG GCC CTG TGC GTG										372 433
S F P O P C R A A E R L O V L L T Y R V										144
TCC TTC CCG CAG CCC TGC CGC GCC GCC GAG CGC CTC CAG GTG CTG CTC ACC TAC CGC GTC										432 493
G E G P G V C W L A P E O T A G K K K P										164
GGG GAG GGA CCC GGG GTT TGC TGG TTG GCT CCC GAG CAG ACA GCA GGA AAG AAG AAG CCC										492 553
F V Y T O G O A V L N R A F F P C F D T										184
TTC GTG TAC ACC CAG GGC CAG GCT GTC CTA AAC CGG GCC TTC TTC CCT TGC TTC GAC ACG										552 613
P A V K Y K Y S A L I E V P D G F T A V										204
CCT GCT GTT AAA TAC AAG TAT TCA GCT CTT ATT GAG GTC CCA GAT GGC TTC ACA GCT GTG										612 673
M S A S T W E K R G P N K F F F O M C O										224
ATG AGT GCT AGC ACC TGG GAG AAG AGA GGT CCA AAT AAG TTC TTC TTC CAG ATG TGT CAG										672 733
P I P S Y L I A L A I G D L V S A E V G										244
CCC ATC CCC TCC TAT CTG ATA GCT TTG GCC ATC GGA GAT CTG GTT TCG GCT GAA GTT GGA										732 793
P R S R V W A E P C L I D A A N E E Y N										264
CCC AGG AGC CGG GTG TGG GCT GAG CCC TGC CTG ATT GAT GCT GCC AAT GAG GAG TAC AAC										792 853
G V I E E F L A T G E K L F G P Y V W G										284
GGG GTG ATA GAA GAA TTT TTG GCA ACA GGA GAG AAG CTT TTT GGA CCT TAT GTT TGG GGA										852 913
R Y D L L F M P P S F P F G G M E N P C										304
AGG TAT GAC TTG CTC TTC ATG CCA CCG TCC TTT CCA TTT GGA GGA ATG GAG AAC CCT TGT										912 973
L T F V T P C L A G D R S L A D V I I										324
CTG ACC TTT GTC ACC CCC TGC CTG CTA GCT GGG GAC CGC TCC TTG GCA GAT GTC ATC ATC										972 1033
H E I S H S W F G N L V T N A N W G E F										344
CAT GAG ATC TCC CAC AGT TGG TTT GGG AAC CTG GTC ACC AAC GCC AAC TGG GGT GAA TTC										1032 1093
W L N E G F T M Y A O R R I S T I L F G										364
TGG CTC AAT GAA GGT TTC ACC ATG TAC GCC CAG AGG AGG ATC TCC ACC ATC CTC TTT GGC										1092 1153
A A Y T C L E A A T G R A L L R O H M D										384
GCT GCG TAC ACC TGC TTG GAG GCT GCA ACG GGG CGG GCT CTG CTG CGT CAA CAC ATG GAC										1152 1213
I T G E E N P L N K L R V K I E P G V D										404
ATC ACT GGA GAG GAA AAC CCA CTC AAC AAG CTC CGC GTG AAG ATT GAA CCA GGC GTT GAC										1212 1273
P D D T Y N E T P Y E K G F C F V S Y L										424
CCG GAC GAC ACC TAT AAT GAG ACC CCC TAC GAG AAA GGT TTC TGC TTT GTC TCA TAC CTG										1272 1333
A H L V G D O D O F D S F L K A Y V H E										444
GCC CAC TTG GTG GGT GAT CAG GAT CAG TTT GAC AGT TTT CTC AAG GCC TAT GTG CAT GAA										1332 1393
F K F R S I L A D D F L D F Y L E Y F P										464
TTC AAA TTC CGA AGC ATC TTA GCC GAT GAC TTT CTG GAC TTC TAC TTG GAA TAT TTC CCT										1392 1453

FIG. 1A.

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E	L	K	K	K	R	V	D	I	I	P	G	F	E	F	D	R	W	L	N	484
GAG	CTT	AAG	AAA	AAG	AGA	GTG	GAT	ATC	ATT	CCA	GGT	TTT	GAG	TTT	GAT	CGA	TGG	CTG	AAT	1452 1513
T	P	G	W	P	P	Y	L	P	D	L	S	P	G	D	S	L	M	K	P	504
ACC	CCC	GGC	TGG	CCC	CCG	TAC	CTC	CCT	GAT	CTC	TCC	CCT	GGG	GAC	TCA	CTC	ATG	AAG	CCT	1512 1573
A	E	E	L	A	O	L	W	A	A	E	E	L	D	M	K	A	I	E	A	524
GCT	GAA	GAG	CTA	GCC	CAA	CTG	TGG	GCA	GCC	GAG	GAG	CTG	GAC	ATG	AAG	GCC	ATT	GAA	GCC	1572 1633
V	A	I	S	P	W	K	T	Y	O	L	V	Y	F	L	D	K	I	L	O	544
GTG	GCC	ATC	TCT	CCC	TGG	AAG	ACC	TAC	CAG	CTG	GTC	TAC	TTC	CTG	GAT	AAG	ATC	CTC	CAG	1632 1693
K	S	P	L	P	P	G	N	V	K	K	L	G	D	T	Y	P	S	I	S	564
AAA	TCC	CCT	CTC	CCT	CCT	GGG	AAT	GTG	AAA	AAA	CTT	GGA	GAC	ACA	TAC	CCA	AGT	ATC	TCA	1692 1753
N	A	R	N	A	E	L	R	L	R	W	G	O	I	V	L	K	N	D	H	584
AAT	GCC	CGG	AAT	GCA	GAG	CTC	CGG	CTG	CGA	TGG	GGC	CAA	ATC	GTC	CTT	AAG	AAC	GAC	CAC	1752 1813
O	E	D	F	W	K	V	K	E	F	L	H	N	O	G	K	O	R	Y	T	604
CAG	GAA	GAT	TTC	TGG	AAA	GTG	AAG	GAG	TTC	CTG	CAT	AAC	CAG	GGG	AAG	CAG	AAG	TAT	ACA	1812 1873
L	P	L	Y	H	A	M	M	G	G	S	E	V	A	O	T	L	A	K	E	624
CTT	CCG	CTG	TAC	CAC	GCA	ATG	ATG	GGT	GGC	AGT	GAG	GTG	GCC	CAG	ACC	CTC	GCC	AAG	GAG	1872 1933
T	F	A	S	T	A	S	O	L	H	S	N	V	V	N	Y	V	O	O	I	644
ACT	TTT	GCA	TCC	ACC	GCC	TCC	CAG	CTC	CAC	AGC	AAT	GTT	GTC	AAC	TAT	GTC	CAG	CAG	ATC	1932 1993
V	A	P	K	G	S	*														651
GTG	GCA	CCC	AAG	GGC	AGT	TAG														1953

AGGCTCGTGTGCATGGCCCTGCCTCTTCAGGCTCTCCAGGCTTTTCTAGATAATTGTTTGTTCCTTCCAAATTCCTGTTCCC  
 TGATCAACTTCCTGGAGTTTATATCCCTCAGGATAATCTATTCTCTAGCTTAGGTATCTGTGACTCTTGGGCTCTGC  
 TCTGGTGGGAACCTTCTCTATAGCCCACTGAGCCCCGAGACAGAGAACCTGCCACAGCTCTCCCGCTACAGGCT  
 GCAGGCACTGCAGGGCAGCGGTATTCTCTCCCACTAAGTCTCTGGGAAGAAGTGAGAGGACTGATGCTCTTCTT  
 TTTCTCTTCTGTCTTTTCTTGTGATTTTATGCAAGGGCTGGCATTCTGATTGTTCTTTTTCAGGTTTAAATCC  
 TTATTTTAATAAAGTTTCAAGCAAAAATTAATAAAAAAAAAAAAAAAAAAAAAA

FIG. 1B.

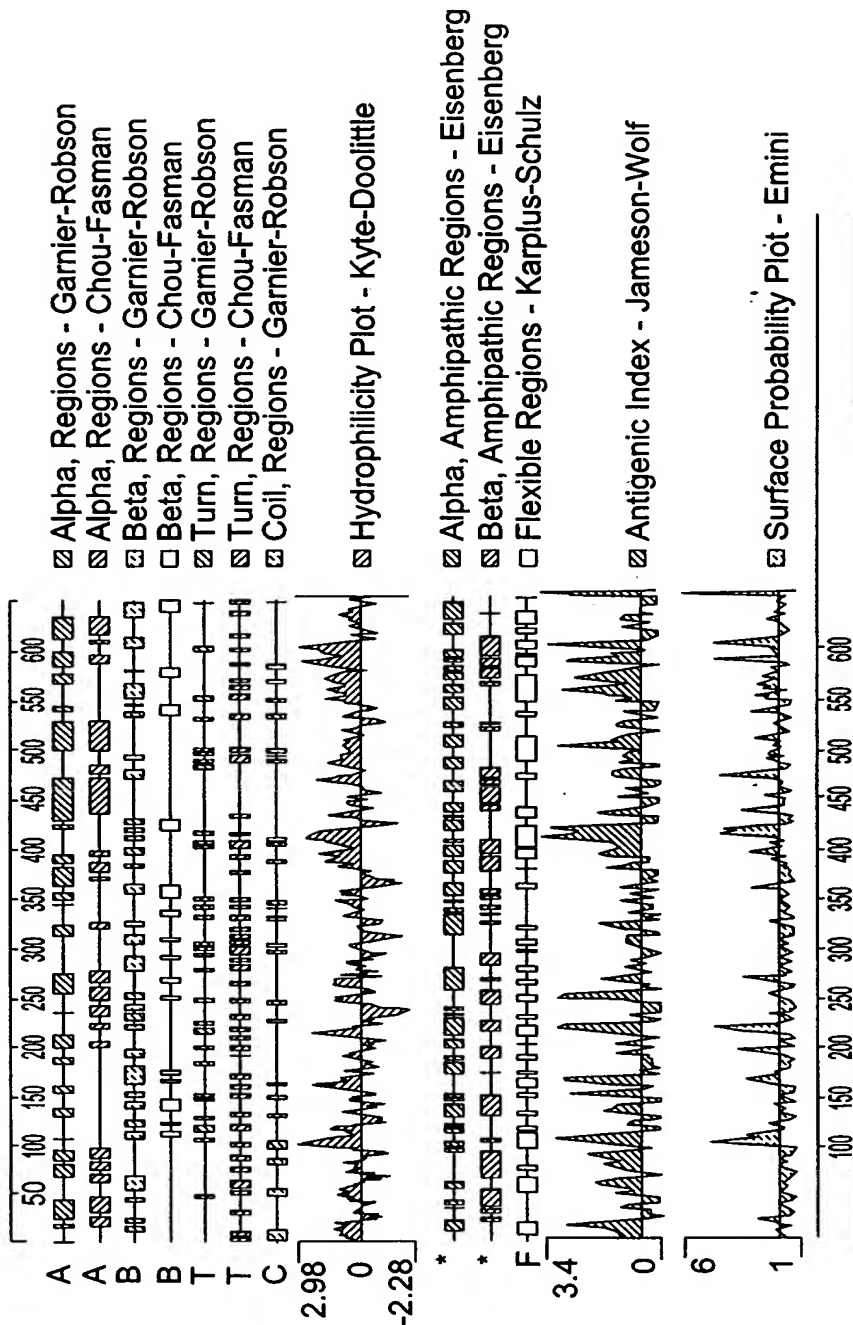
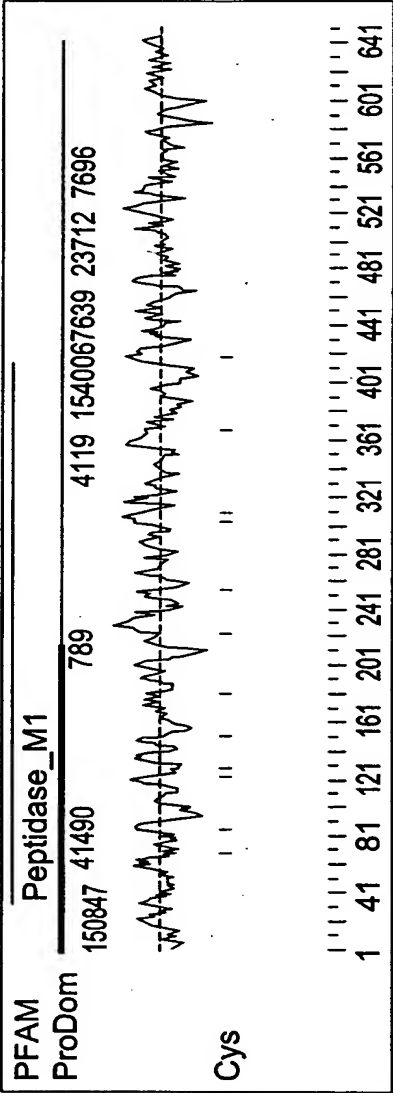


FIG. 2.

Title: 2786, A Novel Human Aminopeptidase  
Inventor(s): Kapeller-Libermann et al.  
Application No: Not Assigned  
Atty Dkt No: 35800/242128(5800-62B)

Analysis of 2786 (650 aa)



**FIG. 3.**

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#### Prosite Pattern Matches for 2786

Prosite version: Release 12.2 of February 1995

>PS00004/PDOC00004/CAMP\_PHOSPHO\_SITE cAMP- and cGMP-dependent protein kinase phosphorylation site.

Query: 356 RRIS 359

>PS00005/PDOC00005/PKC\_PHOSPHO\_SITE Protein kinase C phosphorylation site.

Query: 141.. TYR 143

Query: 374 TGR 376

>PS00006/PDOC00006/CK2\_PHOSPHO\_SITE Casein kinase II phosphorylation site.

Query: 208 STWE 211

#### Analysis of 2786

Query: 318 SLAD 321

Query: 368 TCLE 371

Query: 386 TGEE 389

Query: 408 TYNE 411

Query: 412 TPYE 415

Query: 496 SPGD 499

>PS00008/PDOC00008/MYRISTYL N-myristoylation site.

Query: 9 GSGAAR 14

Query: 58 GLSGTA 63

Query: 119 GQALCV 124

Query: 333 GNLVTN 338

Query: 364 GAAYTC 369

Query: 614 GSEVAQ 619

>PS00009/PDOC00009/AMIDATION Amidation site.

Query: 159 AGKK 162

>PS00030/PDOC00030/RNP\_1 Eukaryotic putative RNA-binding region RNP-1 signature.

Query: 416 KGFCFVS 423

>PS00142/PDOC00129/ZINC\_PROTEASE Neutral zinc metalloproteinases, zinc-binding region signature.

Query: 322 VIIHEISHSW 331

**FIG. 4.**

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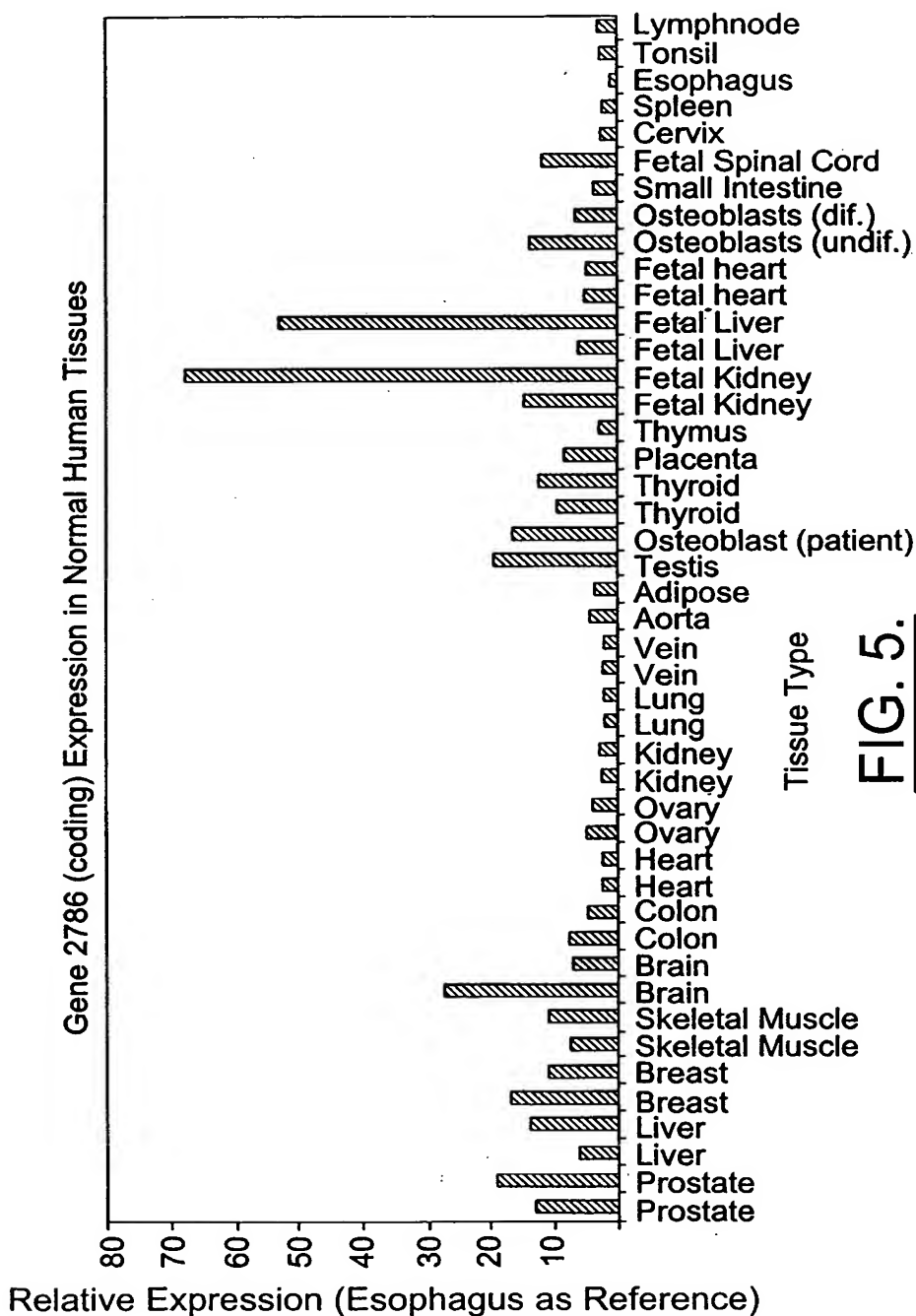


FIG. 5.

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Title: 2786, A Novel Human Aminopeptidase  
 Inventor(s): Kapeller-Libermann et al.  
 Application No: Not Assigned  
 Atty Dkt No: 35800/242128(5800-62B)

2786 Taqman Oncology Panel

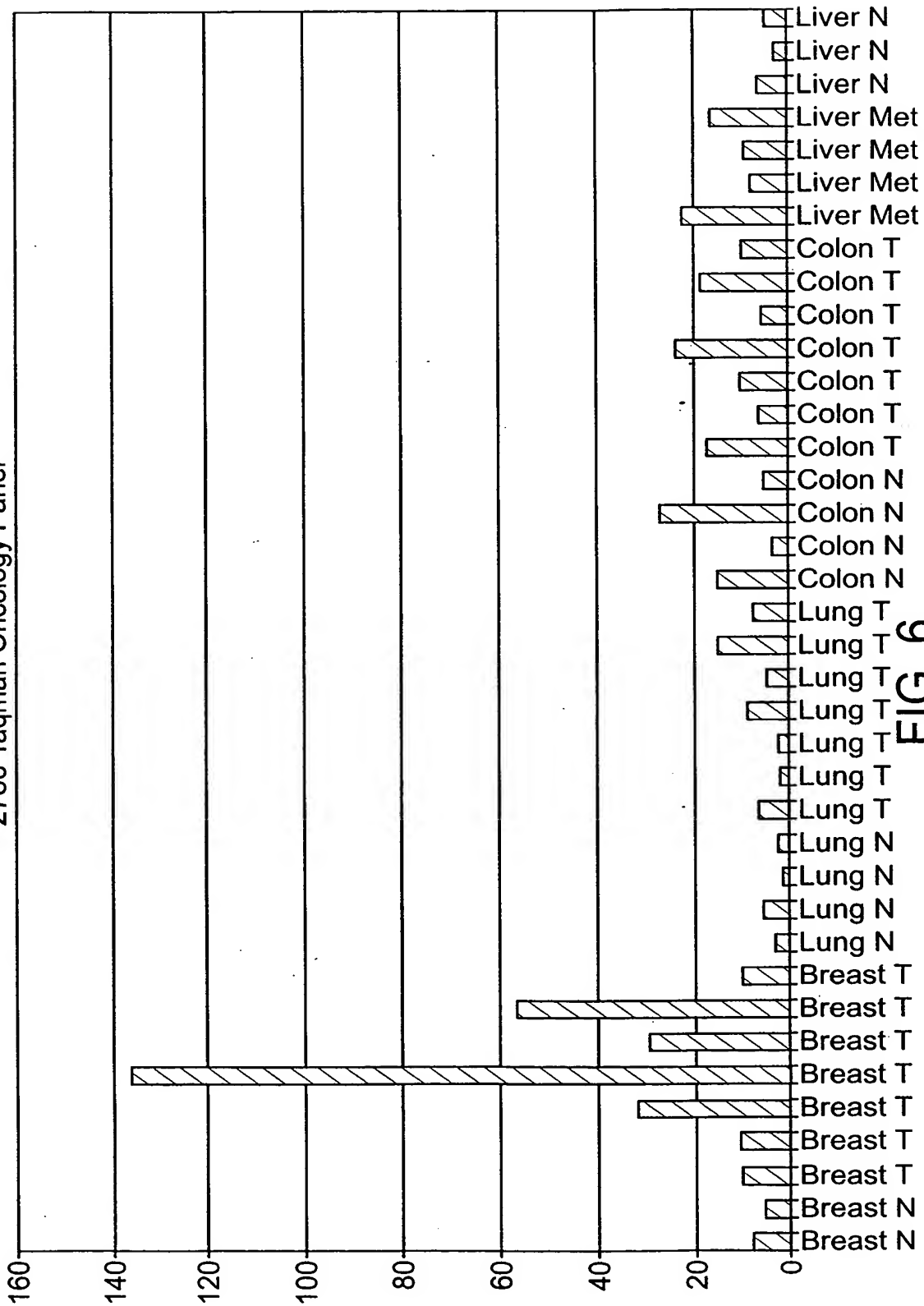


FIG. 6.

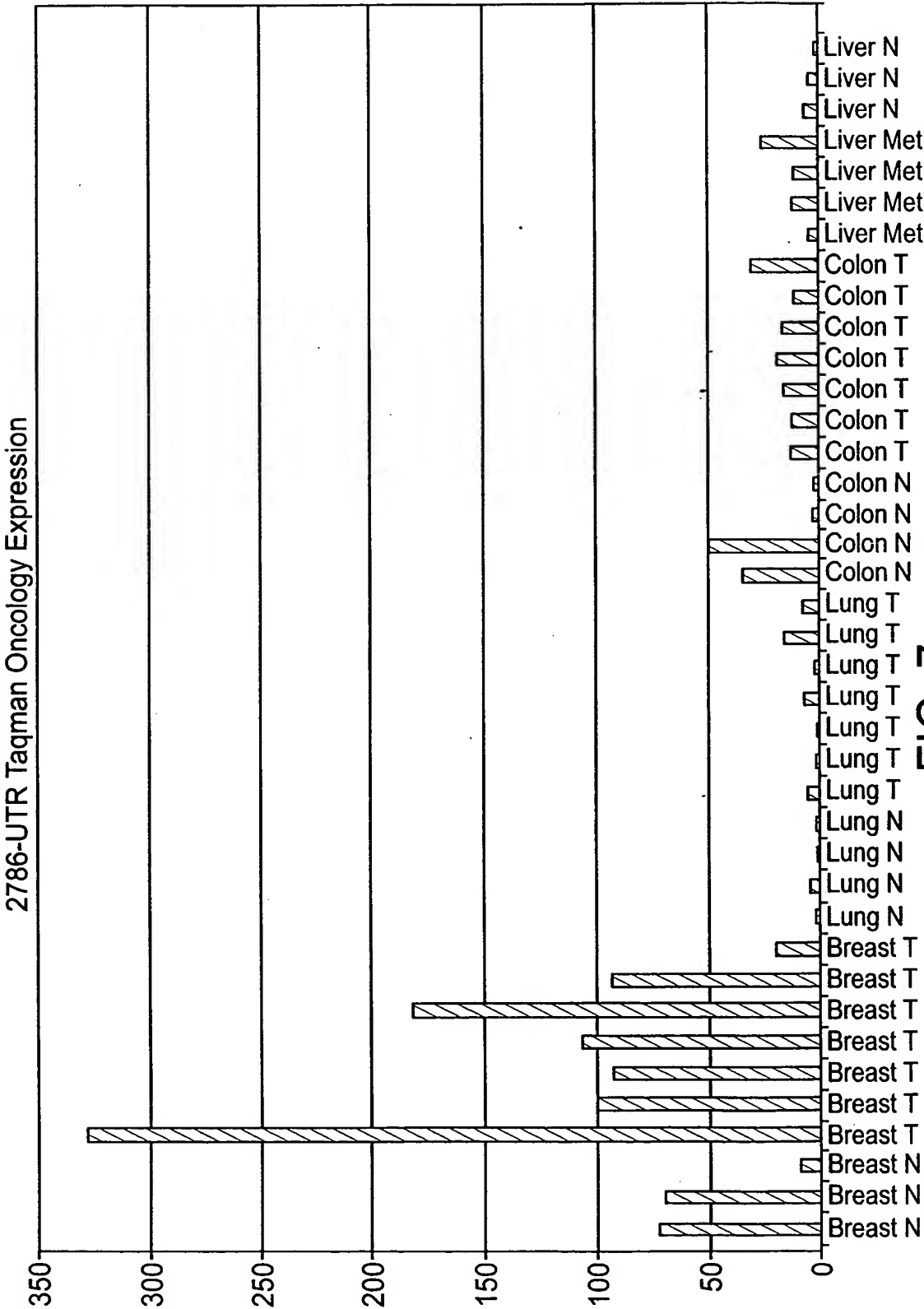


FIG. 7.



Title: 2786, A Novel Human Aminopeptidase  
Inventor(s): Kapeller-Libermann et al.  
Application No: Not Assigned  
Atty Dkt No: 35800/242128(5800-62B)

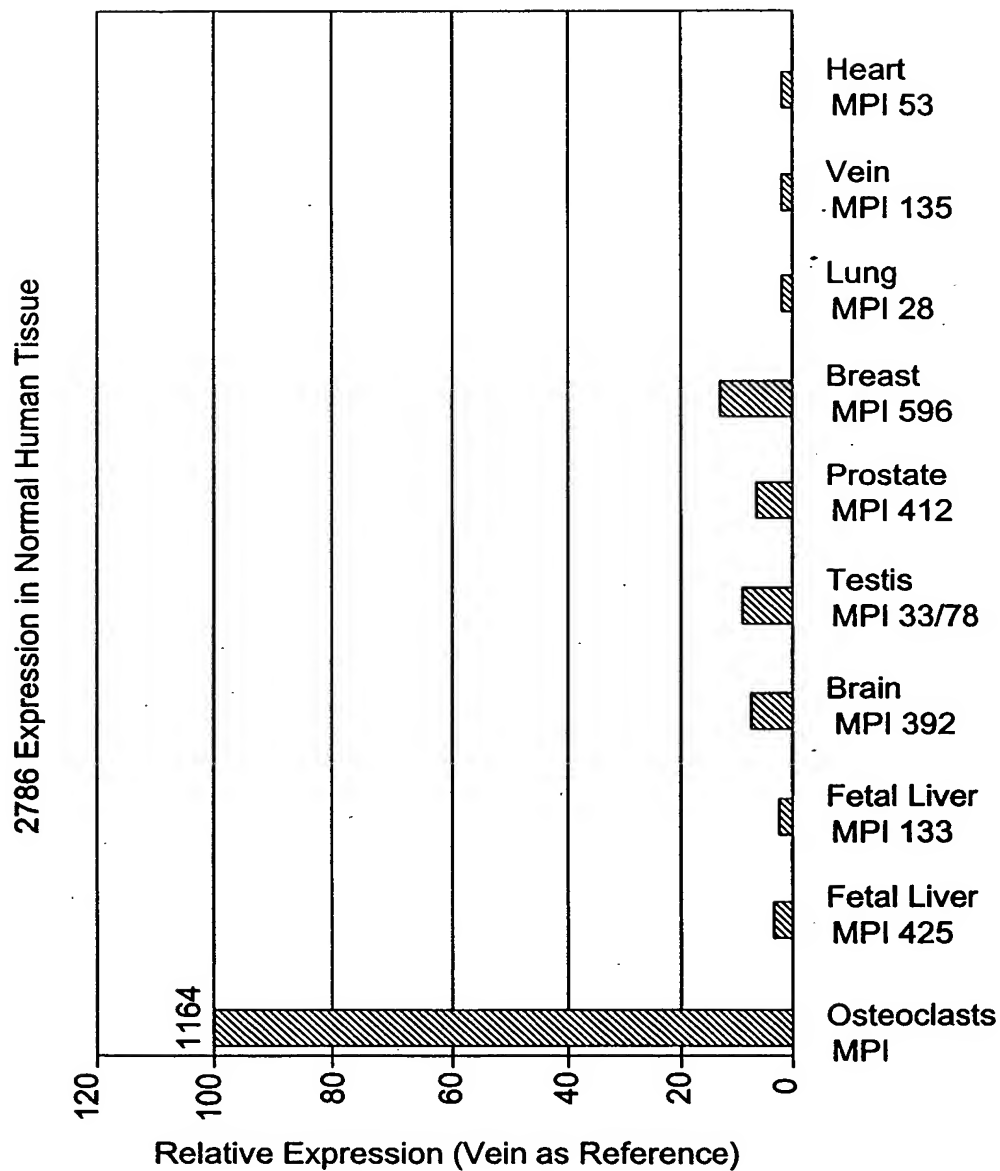


FIG. 8.